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1600

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/502,426A

DATE: 03/13/2003 P.6
TIME: 13:52:27

Input Set : A:\11696-070001.txt

Output Set: N:\CRF4\03132003\I502426A.raw

```

4 <110> APPLICANT: AZPIROZ, Ricardo
5     CHOE, Sunghwa
6     FELDMANN, Kenneth
8 <120> TITLE OF INVENTION: DWF4 POLYNUCLEOTIDES, POLYPEPTIDES AND USES THEREOF
10 <130> FILE REFERENCE: 2225-0001
12 <140> CURRENT APPLICATION NUMBER: 09/502,426A
13 <141> CURRENT FILING DATE: 2000-02-11
15 <150> PRIOR APPLICATION NUMBER: 60/119,657
16 <151> PRIOR FILING DATE: 1999-02-11
18 <150> PRIOR APPLICATION NUMBER: 60/119,658
19 <151> PRIOR FILING DATE: 1999-02-11
21 <160> NUMBER OF SEQ ID NOS: 25
23 <170> SOFTWARE: FastSEQ for Windows Version 4.0
25 <210> SEQ ID NO: 1
26 <211> LENGTH: 6888
27 <212> TYPE: DNA
28 <213> ORGANISM: Arabidopsis sp.
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32 tattctgttc acatgatttg agtttggttc tcaatttgga ttccaagata attaaatatt 120
33 aaaattcatt taaaatattt acaagtaatt aattatcttt acattgtatt gttataacaa 180
34 aatatctatc tttggtatat gagaaaatat ggagtttgga atttataata ataaaggaaa 240
35 taatcgattc catttggttg gattacacag ttaagttttt gtgtttcttt tgttatatgt 300
36 atatgagtaa atcaaaaaga gtattgattg aagtgtaaac atatttcggt atgaccccca 360
37 aaaaaaaaaa aaaaacaaac aaacaaaccc ccccccgat atagtttttg gttctggatt 420
38 aggtttattt gatcataatt acatgcatca tttctttgat tactatgaag attttcttac 480
39 caattaaaat ttcgaattca tatctcttga ttattaaatt aaatacgagt gtgaatatcc 540
40 gtttatcgat cactccaatc atgattatga ttcttgtgct aatccagcaa attattaaca 600
41 agagtattga gaaaaaacg gaaaataagaa aagggaagaa gtagtgaccc atggagtatg 660
42 tgaataatta tcaaagagaa taagagatga caaccaaag gttgtggaat aatggtcctt 720
43 gccagctttc tctcacaatc aatatcgacc ctatttggat tttctggata ttcgttaaaa 780
44 tttgcgataa cgattgtgaa aaataattta tttgttagct gatctcaata ttatgttcca 840
45 ggtatttgca taatcttctg tttaaagcat attttgtctt tctttttgtt tctgtttctt 900
46 taactatata ttatcgcgga tatatgataa caatgatata tcacaaaaca attgtctggg 960
47 accattttga ataaactttt tctcaaacat tacgggacac tggactcgac ccttaaaaata 1020
48 cgattttaca gcgtcactag ttgagattac tagcataaag cataaaggac ccgttcaagc 1080
49 tattttatca aagttacaaa ctgaatatag cttgaaatcc tttagaaaat tttggaatta 1140
50 ccggttggtt tgtaaatata gatttagtgg taaacaaata tgtaaatcaa ttagtgggtca 1200
51 acatatacat aattccttac agaaaaaaca aacttaagag aagttaacat atccatatat 1260
52 gggtagtcta tacctttcac gtatgctata ctagagacta aagaatagtt atgtgatgtc 1320
53 gataaatgaa attcacacgc gtggttaataa ttatgggacc gtatgttacg atcactgcaa 1380
54 atatcattct tgggttggtca acaataaaaa caaaaacaag aaaaaaagaa aacgattttt 1440
55 cttggattcc attcaatgat ctaaaatgca tagatctttt gggttacagt ttcgaagtcc 1500

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56 tctacaagcg tgtaaccatc tgcaactatt aaattgcttt ctttaattgca tctttaacat 1560
57 atttattgtt agttggaatt taataagagc gaacttgtaa cattacaata tttatattag 1620
58 atactagtat gtgattattc caaatacata ctttgatgtt ttaaacttaa tcttgtttct 1680
59 tcctacggtg taaatattaa tcactcgaggt aaaaaaagtt ttgtcttatt ttcgcatg 1740
60 atgaaggata aacctaataa ctttaatttt ttgaaaatgt aaccctttta ctcatagatt 1800
61 aattaccgta tgtttttgtt gccataatga cagcctctac aactgtgata gtcaattttt 1860
62 tctgcaaata ttaaattagg aattcaatgc tactatcaat agaagaaaca gctgagtatt 1920
63 acattttaat ttaaagacaa aatttttgaa aaatgttata atttctaaca atattattaa 1980
64 aatatgatgc ctataatgta tttcctatgt tcttaaaata ttttttttta tatttagtta 2040
65 taaatacatt atgaaccaat aatagttggt gaattcaaat atctccatta atattttttg 2100
66 aaatctacaa attattaata tttagtcaat aacaatgcat agaaagttcc aaaaaaatt 2160
67 ttgttaacag aaacttccaa attttttttt tttatggaac aagaaataac agatagaaaa 2220
68 ctattttgtt gtggaatgga agtagtaata tacattaagc aaatttttaa aaattatata 2280
69 agcctatacg cgctcaaagt atgttatcta gtaggtgtaa ttaataatgc atgggtgcgat 2340
70 tcagaattgg gacaacaatg aaaacggaat taaaatatta actttaaaat aaataaaaat 2400
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73 taggggtcct tctgacattt tcaactgttct acccctactc gtgagccac cttttccca 2580
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79 ctatttcagc atcgacgtt tctgcaactt ttgtttttaa ttaagagtt taataaataa 2940
80 aagtattaaa aggagcataa cgaggcaaca aaagtaatga acacggagaa acaaaagcca 3000
81 tgaagctcat tgggttagttt aagcttaata agaagatttt attaaatttt aatgacgatg 3060
82 ataacaatta ttttttctga cttcttttaa acccctctt acaaacagaa gctccctttt 3120
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84 gagagagaga gaaactagct ccattgttga aacagagcat catactctct tacctcttct 3240
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89 gactaatgtt gtttatttta caggtatggt aagatatata gatcgaactt gtttgagaa 3540
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95 atcttttatt ttgctaaatt tttttgttta gaaatcttta gagtttctaa cttttttttt 3900
96 ttaattgaa cagtttacgt ttaatcta ggcgaagcat ataattgagta tggatcctgg 3960
97 agaagaagaa acagagcaat taaagaaaga gtatgtaact ttcattgaaag gagttgtctc 4020
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99 ttttgctgta aagtcacaaa ctctcattat aggtttttta ttttatttta tgtgttaaat 4140
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102 gaggatgaag cagagatgag taagagtgat catgttagga aacaaagaac agacgatgat 4320
103 cttttgggat gggttttgaa acattcgaat ttatcgacgg agcaaattct cgatctcatt 4380
104 cttagtttgt tatttgccgg acatgagact tcttctgtag ccattgctct cgctatcttc 4440

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105 ttcttgcaag cttgccctaa agccgttgaa gagcttaggg taagataatt ataacagcac 4500
106 aagttaatta ctaccaaatt gttacgtatt atataagtta ttatagaatt attctattag 4560
107 aatatacgat gaaaaaagta tgtatatatta attgtcacta attttatgtt tattgattta 4620
108 tacttttgaa ggaagagcat cttgagatcg cgagggccaa gaaggaacta ggagagtcag 4680
109 aattaaattg ggatgattac aagaaaatgg actttactca atgtgtatgt tactatcatt 4740
110 ctcattattt attctatgtt catatgattt atgatgaaac caaaattatt gatttttttt 4800
111 ttggtgtgtg tgaaggttat aaatgaaact cttcgattgg gaaatgtagt taggtttttg 4860
112 catcgcaaag cactcaaaga tggtcggtag aaaggtaaaa ctttacgtac aaaattttta 4920
113 aataatgaaa tccggaatat tgaaatctta ttggatgaaa aatattaaaa taattttacat 4980
114 ttcttaatgt tggaaaaaag gatacgatat ccctagtggg tggaaagtgt taccgggtgat 5040
115 ctacgccgta catttgata attctcgta tgaccaacct aatctcttta atccttggag 5100
116 atggcaacag gtaataaaaa agtttctctc gttaactatc gaaaattagt gtatagtttt 5160
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118 agaactatta atctggcaaa aactttttat tattattatc tttcaagtta gatcttaaca 5280
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120 gtgttggtgt aagtgtacgt gaagacaatt aattagtagg atggtatgtc tttaatgacg 5400
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123 atgacttgta cgtgcgttag attctgccac gttgactggt tttataactt agatttataa 5580
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126 tagtgagtgg ggaaggttaag aggtggtgag agatgattaa tgacccacg tgggtggtg 5760
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133 agatgaaagt atttttattc tcttcttttt tttttgataa ttttaaatca ttttttttgc 6180
134 ccaatgatat ataaaaattt ggataaataa tattattgga tattcgtttt ttagttcggg 6240
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144 tcacttttag gatcctcttc tagacgagta aagtaatcct cgttaccaag caatggtctc 6840
145 atcttttgaa gacaggtctt ttccaagtcc tagttcaggc caaagctt 6888

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147 <210> SEQ ID NO: 2

148 <211> LENGTH: 513

149 <212> TYPE: PRT

150 <213> ORGANISM: Arabidopsis sp.

152 <400> SEQUENCE: 2

153 Met Phe Glu Thr Glu His His Thr Leu Leu Pro Leu Leu Leu Leu Pro

154 1 5 10 15

156 Ser Leu Leu Ser Leu Leu Leu Phe Leu Ile Leu Leu Lys Arg Arg Asn

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157          20          25          30
158 Arg Lys Thr Arg Phe Asn Leu Pro Pro Gly Lys Ser Gly Trp Pro Phe
159          35          40          45
161 Leu Gly Glu Thr Ile Gly Tyr Leu Lys Pro Tyr Thr Ala Thr Thr Leu
162          50          55          60
164 Gly Asp Phe Met Gln Gln His Val Ser Lys Tyr Gly Lys Ile Tyr Arg
165 65          70          75          80
167 Ser Asn Leu Phe Gly Glu Pro Thr Ile Val Ser Ala Asp Ala Gly Leu
168          85          90          95
170 Asn Arg Phe Ile Leu Gln Asn Glu Gly Arg Leu Phe Glu Cys Ser Tyr
171          100          105          110
173 Pro Arg Ser Ile Gly Gly Ile Leu Gly Lys Trp Ser Met Leu Val Leu
174          115          120          125
176 Val Gly Asp Met His Arg Asp Met Arg Ser Ile Ser Leu Asn Phe Leu
177          130          135          140
179 Ser His Ala Arg Leu Arg Thr Ile Leu Leu Lys Asp Val Glu Arg His
180 145          150          155          160
182 Thr Leu Phe Val Leu Asp Ser Trp Gln Gln Asn Ser Ile Phe Ser Ala
183          165          170          175
185 Gln Asp Glu Ala Lys Lys Phe Thr Phe Asn Leu Met Ala Lys His Ile
186          180          185          190
188 Met Ser Met Asp Pro Gly Glu Glu Glu Thr Glu Gln Leu Lys Lys Glu
189          195          200          205
191 Tyr Val Thr Phe Met Lys Gly Val Val Ser Ala Pro Leu Asn Leu Pro
192          210          215          220
194 Gly Thr Ala Tyr His Lys Ala Leu Gln Ser Arg Ala Thr Ile Leu Lys
195 225          230          235          240
197 Phe Ile Glu Arg Lys Met Glu Glu Arg Lys Leu Asp Ile Lys Glu Glu
198          245          250          255
200 Asp Gln Glu Glu Glu Glu Val Lys Thr Glu Asp Glu Ala Glu Met Ser
201          260          265          270
203 Lys Ser Asp His Val Arg Lys Gln Arg Thr Asp Asp Asp Leu Leu Gly
204          275          280          285
206 Trp Val Leu Lys His Ser Asn Leu Ser Thr Glu Gln Ile Leu Asp Leu
207          290          295          300
209 Ile Leu Ser Leu Leu Phe Ala Gly His Glu Thr Ser Ser Val Ala Ile
210 305          310          315          320
212 Ala Leu Ala Ile Phe Phe Leu Gln Ala Cys Pro Lys Ala Val Glu Glu
213          325          330          335
215 Leu Arg Glu Glu His Leu Glu Ile Ala Arg Ala Lys Lys Glu Leu Gly
216          340          345          350
218 Glu Ser Glu Leu Asn Trp Asp Asp Tyr Lys Lys Met Asp Phe Thr Gln
219          355          360          365
221 Cys Val Ile Asn Glu Thr Leu Arg Leu Gly Asn Val Val Arg Phe Leu
222          370          375          380
224 His Arg Lys Ala Leu Lys Asp Val Arg Tyr Lys Gly Tyr Asp Ile Pro
225 385          390          395          400
227 Ser Gly Trp Lys Val Leu Pro Val Ile Ser Ala Val His Leu Asp Asn
228          405          410          415

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230 Ser Arg Tyr Asp Gln Pro Asn Leu Phe Asn Pro Trp Arg Trp Gln Gln
231                420                425                430
233 Gln Asn Asn Gly Ala Ser Ser Ser Gly Ser Gly Ser Phe Ser Thr Trp
234                435                440                445
236 Gly Asn Asn Tyr Met Pro Phe Gly Gly Gly Pro Arg Leu Cys Ala Gly
237                450                455                460
239 Ser Glu Leu Ala Lys Leu Glu Met Ala Val Phe Ile His His Leu Val
240 465                470                475                480
242 Leu Lys Phe Asn Trp Glu Leu Ala Glu Asp Asp Gln Pro Phe Ala Phe
243                485                490                495
245 Pro Phe Val Asp Phe Pro Asn Gly Leu Pro Ile Arg Val Ser Arg Ile
246                500                505                510
248 Leu
252 <210> SEQ ID NO: 3
253 <211> LENGTH: 24
254 <212> TYPE: DNA
255 <213> ORGANISM: Artificial Sequence
257 <220> FEATURE:
258 <223> OTHER INFORMATION: Description of Artificial Sequence: primer D4OVERF
260 <400> SEQUENCE: 3
261 atgttcgaaa cagagcatca tact                                24
262 <210> SEQ ID NO: 4
263 <211> LENGTH: 21
264 <212> TYPE: DNA
265 <213> ORGANISM: Artificial Sequence
267 <220> FEATURE:
268 <223> OTHER INFORMATION: Description of Artificial Sequence: primer D4PRM
270 <400> SEQUENCE: 4
271 cctcgatcaa agagagagag a                                21
273 <210> SEQ ID NO: 5
274 <211> LENGTH: 29
275 <212> TYPE: DNA
276 <213> ORGANISM: Artificial Sequence
278 <220> FEATURE:
279 <223> OTHER INFORMATION: Description of Artificial Sequence: primer D4RTF
281 <400> SEQUENCE: 5
282 ttcttggtga aaccatcggt tatcttaaa                        29
284 <210> SEQ ID NO: 6
285 <211> LENGTH: 26
286 <212> TYPE: DNA
287 <213> ORGANISM: Artificial Sequence
289 <220> FEATURE:
290 <223> OTHER INFORMATION: Description of Artificial Sequence: primer D4RTR
292 <400> SEQUENCE: 6
293 tatgataagc agttcctggt agattt                            26
295 <210> SEQ ID NO: 7
296 <211> LENGTH: 21
297 <212> TYPE: DNA
298 <213> ORGANISM: Artificial Sequence

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RAW SEQUENCE LISTING ERROR SUMMARY
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:25; Xaa Pos. 1,2,3,4,5,6,7,8,9,10,11,12,13,14,15,16,17,18,19,20,21,22
Seq#:25; Xaa Pos. 23,24,25,26,27,28,29,30,31,32,33,34,35,36,37,38,42,43,46
Seq#:25; Xaa Pos. 48,50,56,57,58,61,62,63,64,65,66,67,68,72,82,92,93,94,95
Seq#:25; Xaa Pos. 96,97,102,107,108,111,112,113,114,126,128,136,138,142,146
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Seq#:25; Xaa Pos. 184,185,186,190,193,197,201,203,204,206,207,208,209,212
Seq#:25; Xaa Pos. 213,216,217,218,219,221,228,229,230,232,233,236,237,239
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Seq#:25; Xaa Pos. 442,451,459,471,481,484,485,487,488,489,490,494,495,496
Seq#:25; Xaa Pos. 497,498,499,500,501,502,503,505,506,526,535,541,542,543
Seq#:25; Xaa Pos. 545,546,547,551,555,558,566,567,570,571,572,573,574,575

VERIFICATION SUMMARY

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L:844 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:848 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:25
L:849 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:25 after pos.:0
M:341 Repeated in SeqNo=25